

## INFORMATION DISCLOSURE STATEMENT LIST

(Use as many sheets as necessary)

Complete if Known

Application Number	10/634,027
Filing Date	August 4, 2003
First Named Inventor	EVDOKIMOV <i>et al.</i>
Group Art Unit	1656
Examiner Name	Noakes, Suzanne Marie

### U.S. PATENT DOCUMENTS

Examiner's Initials	Cite No.	Document No.	Date	Name	Class	Subclass	Filing Date (if appropriate)

### FOREIGN PATENT DOCUMENTS

Examiner's Initials	Cite No.	Foreign Patent Document Country Code-Number-Kind Code	Date	Name	Translation Yes      No
	B1	WO 00/65088	11/02/2000	Amersham Pharmacia Biotech AB	
	B2	WO 02/26774 A2	04/02/2002	Procter & Gamble Company	

### NON PATENT LITERATURE DOCUMENTS

Examiner's Initials	Cite No.	Non-Patent Citations (include Author, Title, Publisher, Relevant Pages, Date and Place of Publication)
	B3	BARTLETT <i>et al.</i> , "Molecular Recognition in Chemical and Biological Problems," Special Pub., Royal Chem. Soc., 78, 182-196 Caveat: A Program to Facilitate the Structure-derived Design of Biologically Active Molecules (April 1989)
	B4	BÖHM, "The Computer Program LUDI: A New Method for the Novo Design of Enzyme Inhibitors," <i>J. Computer-Aided Molecular Design</i> , 6:61-78 (1992)
	B5	GOODFORD, "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules," <i>J. Med. Chem.</i> , 28(7):849-857 (1985)
	B6	GOODSELL <i>et al.</i> , "Automated Docking of Substrates to Proteins by Simulated Annealing," <i>Proteins: Structure, Function, and Genetics</i> , 8:195-202 (1990)
	B7	JONES <i>et al.</i> , "Molecular Recognition of Receptor Sites Using a Genetic Algorithm with a Description of Desolvation," <i>J. Mol. Biol.</i> , 245:43-53 (1995)
	B8	KRUEGAR <i>et al.</i> , "Structural Diversity and Evolution of Human Receptor-Like Protein Tyrosine Phosphatases," <i>EMBO Journal</i> , 9(10):3241-3252 (1990)
	B9	KUNTZ <i>et al.</i> , "A Geometric Approach to Macromolecule - Ligand Interactions," <i>J. Mol. Biol.</i> , 161:269-288 (1982)
	B10	MARTIN, "3D Database Searching in Drug Design," <i>J. Med. Chem.</i> , 35(12):2145-2154 (1992)
	B11	MIRANKER <i>et al.</i> , "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method," <i>Proteins: Structure, Function and Genetics</i> , 11:29-34 (1991)
	B12	NAVAZA, "AMoRe: An Automated Package for Molecular Replacement," <i>Acta Cryst. A</i> 50:157-163 (1994)
	B13	NISHIBATA <i>et al.</i> , "Automatic Creation of Drug Candidate Structures Based on Receptor Structure. Starting Point for Artificial Lead Generation," <i>Tetrahedron</i> , 47(43):8985-8990 (1991)
	B14	Collaborative Computational Project, Number 4, "The CCP4 Suite: Programs for Protein Crystallography," <i>Acta Cryst.</i> , D50:760-763 (1994)

**Examiner Signature:**

**Date Considered**

EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.